

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/575,361DATE: 06/07/96
TIME: 09:43:18

INPUT SET: S10941.raw

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

(1) GENERAL INFORMATION:

(i) APPLICANT: Chandrasegaran, Srinivasan

(ii) TITLE OF INVENTION: A GENERAL METHOD TO CLONE HYBRID
RESTRICTION ENDONUCLEASES USING lig GENE

(iii) NUMBER OF SEQUENCES: 35

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cushman Darby & Cushman L.L.P.

(B) STREET: 1100 New York Avenue, NW, Ninth Floor, East
Tower

(C) CITY: Washington

(D) STATE: DC

(E) COUNTRY: USA

(F) ZIP: 20005-3918

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/575,361

(B) FILING DATE: 20-DEC-1995

(C) CLASSIFICATION: 435

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kokulis, Paul N.

(B) REGISTRATION NUMBER: 16,773

(C) REFERENCE/DOCKET NUMBER: PNK/4130/213779/DJP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-861-3000

(B) TELEFAX: 202-822-0944

(C) TELEX: 6714627 CUSH

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

format
error
throughout**Explanation of error that occurred throughout the Sequence Listing:**

For all of your nucleic acid and amino acid sequences, the text at the end of each line "wrapped" down to the next line. This occurred if your file was retrieved in a word processor after creating it in PatentIn. Your word processor probably has different margin settings than those used in PatentIn. (A right margin set at least to .3 in your word processor will prevent wrapping). Please submit your original ".app" file that can be found in the /patentin/projects subdirectory.

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/575,361DATE: 06/07/96
TIME: 09:43:21

INPUT SET: S10941.raw

51
52 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
53
54 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
55 Leu 1 5 10 15 Leu
56
57
58
59 Xaa Xaa His Xaa Xaa Xaa His
60 20
61
62 (2) INFORMATION FOR SEQ ID NO:2:
63
64 (i) SEQUENCE CHARACTERISTICS:
65 (A) LENGTH: 24 amino acids
66 (B) TYPE: amino acid
67 (D) TOPOLOGY: linear
68
69
70
71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
72
73 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
74 Leu 1 5 10 15
75
76
77
78 Xaa Xaa His Xaa Xaa Xaa Xaa His
79 20
80
81 (2) INFORMATION FOR SEQ ID NO:3:
82
83 (i) SEQUENCE CHARACTERISTICS:
84 (A) LENGTH: 25 amino acids
85 (B) TYPE: amino acid
86 (D) TOPOLOGY: linear
87
88
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
91
92 Tyr Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa
93 Leu 1 5 10 15
94
95
96
97 Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
98 20 25
99
100 (2) INFORMATION FOR SEQ ID NO:4:

sample of amino acid "wraps"

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/575,361DATE: 06/07/96
TIME: 09:43:47

INPUT SET: S10941.raw

451 (2) INFORMATION FOR SEQ ID NO:23:

452

453 (i) SEQUENCE CHARACTERISTICS:

454 (A) LENGTH: 74 base pairs

455 (B) TYPE: nucleic acid

456 (C) STRANDEDNESS: single

457 (D) TOPOLOGY: linear

458

459

460

461 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

462

463 CUCGACCAAA CCUAGGUUCG AAGGGCCCCU UCUUAAGCUC CUCCGAGAGC UCCAGCUGAA

464

465

466 GGAGAUCCUCC AUGG

467

468

469 (2) INFORMATION FOR SEQ ID NO:24:

470

471 (i) SEQUENCE CHARACTERISTICS:

472 (A) LENGTH: 87 base pairs

473 (B) TYPE: nucleic acid

474 (C) STRANDEDNESS: double

475 (D) TOPOLOGY: linear

476

477

478

479 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

480

481 GGATCCAAAGC TTAGCGATCT GCCTGCAGGT CGACTCTAGC CAGGGGCGGG GTGGTCTAGT

482

483

484 ATCGTTCAAT GATACTTCAT GGAATTC

485

486

487 (2) INFORMATION FOR SEQ ID NO:25:

488

489 (i) SEQUENCE CHARACTERISTICS:

490 (A) LENGTH: 23 base pairs

491 (B) TYPE: nucleic acid

492 (C) STRANDEDNESS: single

493 (D) TOPOLOGY: linear

494

495

496

497 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

498

499 CCCCTGAAGG AGATATACAT ATG

500

Sample of
nucleic acid
wraps.

60

74

60

87

23

Entire
listing
not
shown.
(Just these
two sample
pages)

08/575,361

Notice of Availability

Applicant Aid for Biotechnology Computer Readable Form (CRF) Sequence Listings Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (sequence rules: 37 CFR 1.821 through 1.825). (Final rules were published in the *Federal Register* (55 FR 18230) on May 1, 1990, and in the *PTO Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.)

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

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Cost: Free-of-charge
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Login as "anonymous". Software is in directory /pub/checker
Cost: Free-of-charge
- 3) For diskette copies, telephone requests to 703-306-2600.
Cost: \$25.00

For Further Information Contact: Meredith Beckhardt at 703-308-421